



SEQUENCE LISTING

<110> DYAX Corp.

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Luneau, Christopher J.

Ladner, Robert C

<120> NOVEL ENTEROKINASE CLEAVAGE SEQUENCES

<130> DYX-012.1 US, DYX-012.1 PCT

<140> 09/884,767

<141> 2001-06-19

<150> US 09/597,321

<151> 2000-06-19

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<170> PatentIn version 3.1

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Glu Gly Pro Cys His Pro Gln Phe Pro Arg Cys Tyr Ile Glu Asn Leu  
20 25 30

Asp Glu Phe Arg Pro Gly Gly Ser Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Gly Ala Gln Ser Asp Gly Gly Ser  
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Thr Glu His Ala Glu Gly Gly Ser Ala Asp Pro Ser Tyr Ile Glu Gly  
65 70 75 80

Arg Ile Val Gly Ser Ala  
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Xaa Xaa Xaa Xaa Asp Arg Xaa  
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<213> Artificial Sequence

<220>  
<223> Bacteriophage M13mp18

<400> 212  
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actgtgaaa gttgttagc aaaacccat acagaaaatt catttactaa cgtctggaaa 120  
gacgacaaaa ctttagatcg ttacgctaac tatgagggtt gtctgtggaa tgctacaggc 180  
gtttagttt gtactggtga cgaaaactcag tgttacggta catgggttcc tattggcatt 240  
gctatccctg aaaatgaggg tggggctct gagggggcg gttctgaggg tggcggttct 300  
gagggggcg gtactaaacc tcctgagtcg ggtgatacac ctattccggg ctataacttat 360  
atcaaccctc tcgacggcac ttatccgcct ggtactgagc aaaacccgc taatcctaatt 420  
ccttctcttggaggactca gcctcttaat actttcatgt ttcagaataa taggttccga 480  
aataggcagg gggcattaac tgtttatacg ggcactgtta ctcaaggcac tgacccgtt 540  
aaaacttatt accagtacac tcctgtatca tcaaaagcca tgtatgacgc ttactggAAC 600  
ggtaaattca gagactgcgc tttccattct ggctttaatg aagatccatt cgtttgaa 660  
tatcaaggcc aatcgcttga cctgcctcaa cctcctgtca atgctggcg cggtctgggt 720  
ggtggttctg gtggcggttc tgagggtggt ggctctgagg gtggcggttc tgagggtggc 780

ggctctgagg gaggcggggtc cggtggtggc tctggttccg gtgattttga ttatgaaaag 840  
atggcaaaacg ctaataaggg ggctatgacc gaaaatgccg atgaaaacgc gctacagtct 900  
gacgctaaag gcaaacttga ttctgtcgct actgattacg gtgctgctat cgatggttc 960  
attggtgacg tttccggcct tgctaattggt aatggtgcta ctggtgattt tgctggctct 1020  
aattccaaa tggctcaagt cggtgacggt gataattcac ctttaatgaa taattccgt 1080  
caatatttac cttccctccc tcaatcggtt gaatgtcgcc cttttgtctt tagcgctgg 1140  
aaaccatatg aattttctat tgattgtgac aaaataaact tattccgtgg tgtctttgcg 1200  
tttctttat atgttgcac ctttatgtat gtatttcta cgtttgctaa catactgcgt 1260  
aataaggagt ct 1272

<210> 213  
<211> 424  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Bacteriophage M13mp18

<400> 213

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser  
1 5 10 15

His Ser Ala Glu Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu  
20 25 30

Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr  
35 40 45

Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys  
50 55 60

Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu  
65 70 75 80

Ala Ile Pro Glu Asn Glu Gly Gly Ser Glu Gly Gly Ser Glu  
85 90 95

Gly Gly Gly Ser Glu Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp  
100 105 110

Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr  
115 120 125

Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu  
130 135 140

Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg  
145 150 155 160

Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly  
165 170 175

Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys  
180 185 190

Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe  
195 200 205

His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln  
210 215 220

Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Ser Gly  
225 230 235 240

Gly Gly Ser Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly  
245 250 255

Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Gly Ser Gly  
260 265 270

Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala  
275 280 285

Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly  
290 295 300

Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe  
305 310 315 320

Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp  
325 330 335

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn  
340 345 350

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln  
355 360 365

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu  
370 375 380

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala  
385 390 395 400

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala  
405 410 415

Asn Ile Leu Arg Asn Lys Glu Ser  
420

<210> 214  
<211> 957  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Bacteriophage M13mp18  
  
<400> 214  
aaacctcctg agtacggta tacacctatt ccgggctata cttatatcaa ccctctcgac 60  
ggcacttatac cgccctggta ctagcaaaac cccgctaatac ctaatccttc tcttgaggag 120  
tctcagcctc ttaatacttt catgttttag aataataggt tccgaaatag gcagggggca 180  
ttaactgttt atacgggcac tggtaactcaa ggcactgacc ccgttaaaac ttattaccag 240  
tacactcctg tatcatcaaa agccatgtat gacgcttact ggaacggtaa attcagagac 300  
tgcgctttcc attctggctt taatgaagat ccattcgttt gtgaatatac aggccaatcg 360  
tctgacctgc ctcaacctcc tgtcaatgct ggccggggct ctgggtgggg ttctgggtgc 420  
ggctctgagg gtgggtggctc tgagggtggc ggttctgagg gtggcggctc tgagggaggc 480  
ggttccggtg gtggctctgg ttccggtgat tttgattatg aaaagatggc aaacgcta 540  
aagggggcta tgaccgaaaa tgccgatgaa aacgcgctac agtctgacgc taaaggcaaa 600  
cttgattctg tcgctactga ttacggtgct gctatcgatg gttcattgg tgacgtttcc 660  
ggccttgcta atggtaatgg tgctactgg gatggctg gctctaattc ccaaatggct 720

caagtcggtg acggtgataa ttcacctta atgaataatt tccgtcaata tttaccttc 780  
ctccctcaat cggttgaatg tcgcccttt gtcttagcg ctggtaaacc atatgaattt 840  
tctattgatt gtgacaaaat aaacttattc cgtggtgtct ttgcgttct tttatatgtt 900  
gccacctta tgtatgtatt ttctacgttt gctaacatac tgcgtaataa ggagtct 957

<210> 215  
<211> 319  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Bacteriophage M13mp18

<400> 215

Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr Ile  
1 5 10 15

Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala  
20 25 30

Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met  
35 40 45

Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr  
50 55 60

Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln  
65 70 75 80

Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly  
85 90 95

Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe  
100 105 110

Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val  
115 120 125

Asn Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Gly  
130 135 140

Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly  
145 150 155 160

Gly Ser Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met  
165 170 175

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala  
180 185 190

Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr  
195 200 205

Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn  
210 215 220

Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala  
225 230 235 240

Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln  
245 250 255

Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe  
260 265 270

Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn  
275 280 285

Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met  
290 295 300

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser  
305 310 315

<210> 216

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> Bacteriophage M13mp18

<400> 216  
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gaaaacgcgc tacagtctga cgctaaaggc aaacttgatt ctgtcgctac tgattacggt 120

gctgctatcg atggtttcat tggtgacggtt tccggccttg ctaatggtaa tggtgctact 180

ggtgattttg ctggctctaa ttcccaaatg gctcaagtcg gtgacggta taattcacct 240  
ttaatgaata atttccgtca atatttacct tccctccctc aatcggttga atgtcgccct 300  
tttgtcttta gcgctggtaa accatatgaa ttttctattg attgtgacaa aataaaactta 360  
ttccgtggtg tctttgcgtt tctttatat gttgccacct ttatgtatgt atttctacg 420  
tttgctaaca tactgcgtaa taaggagtct 450

<210> 217  
<211> 150  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Bacteriophage M13mp18

<400> 217

Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr  
1 5 10 15

Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu  
20 25 30

Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly  
35 40 45

Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala  
50 55 60

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro  
65 70 75 80

Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val  
85 90 95

Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser  
100 105 110

Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu  
115 120 125

Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile  
130 135 140

Leu Arg Asn Lys Glu Ser  
145 150